

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:21:53 ; Search time 45.33 seconds

(without alignments)
163.223 Million cell updates/sec

Title: US-09-351-778a-11

Perfect score: 77

Sequence: 1 MTGGTIAPTDYNRTATG.....LICCKRRRARRPSELLQYD 77

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 9609334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	31.2	93	1 ERAD53	early E3A 10.5K pr
2	7	9.1	69	2 E58888	H+-transporting AT
3	7	9.1	110	2 D72863	Acort-107 protein
4	7	9.1	160	2 C93413	hypothetical prote
5	7	9.1	197	2 C86523	Ct142 hypothetical
6	7	9.1	249	2 T41847	ACMNPV orf106 - Bo
7	7	9.1	387	2 C89783	hypothetical prote
8	7	9.1	391	2 D97201	atCAR transformat
9	7	9.1	425	2 AC2909	MFS permease (Im
10	7	9.1	487	2 B97684	probable tartrate
11	7	9.1	536	2 T27668	hypothetical prote
12	7	9.1	965	2 T17395	hypothetical prote
13	7	9.1	1175	2 H83437	probable DEAH ATP-
14	7	9.1	1401	2 T17452	hypothetical prote
15	7	9.1	1401	2 T30247	Werner syndrome pr
16	7	7.8	69	2 PN0453	adenylate cyclase
17	7	7.8	79	2 T44145	B2 protein (Import
18	7	7.8	83	2 G82744	hypothetical prote
19	7	7.8	89	2 D87338	hypothetical prote
20	7	7.8	94	2 E82529	phage-related prot
21	7	7.8	94	2 D82526	conserved hypothet
22	7	7.8	97	2 C81102	hypothetical prote
23	7	7.8	97	2 T40639	hypothetical prote
24	7	7.8	106	2 D89473	protein F52D2.5 (1
25	7	7.8	113	2 C81220	hypothetical prote
26	7	7.8	113	2 G81990	hypothetical prote
27	7	7.8	119	2 H83186	hypothetical prote
28	7	7.8	121	2 J01646	nucleic acid-bind
29	7	7.8	126	2 D95915	hypothetical prote

30	6	7.8	128	2 AD1054	conserved hypothet
31	6	7.8	130	2 E70353	hypothetical prote
32	6	7.8	134	2 S52546	thionin variant Th
33	6	7.8	135	2 S12549	hypothetical prote
34	6	7.8	136	2 T23996	hypothetical prote
35	6	7.8	142	2 S32960	hypothetical prote
36	6	7.8	144	2 A53588	hypothetical prote
37	6	7.8	148	2 T03569	high-affinity dram
38	6	7.8	149	2 E70753	hypothetical prote
39	6	7.8	150	2 G87270	general secretion
40	6	7.8	157	2 S75191	hypothetical prote
41	6	7.8	157	2 S35037	hypothetical prote
42	6	7.8	157	2 T48683	heliix-loop-helix p
43	6	7.8	161	2 S52600	hypothetical prote
44	6	7.8	161	2 S53473	probable membrane
45	6	7.8	170	2 T17286	probable membrane

ALIGNMENTS

RESULT 1
ERAD53
early E3A 10.5K protein - human adenovirus 5
C:Species: Mastadenovirus h5 (human adenovirus 5)
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C:Accession: A05245
R:Cladarias, C.; Wold, W.S.M.
Virology 140, 28-43, 1985
A:Title: DNA sequence of the early E3 transcription unit of adenovirus 5.
A:Reference number: A94335; MUID:85092388
A:Accession: A05245
A:Molecule type: DNA
A:Residues: 1-93 <CIA>
A:Cross-references: GB:X03002; NID:958503; PIDN:CAA26784.1; PID:958507
C:Superfamily: adenovirus early E3A 10.5K protein
C:Keywords: early protein; transmembrane protein

Query Match 31.2% Score 24; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMWFSIALMFVCLIIIMLICLKR 64
DB 34 MMWFSIALMFVCLIIIMLICLKR 57

RESULT 2
E58888
H+-transporting ATP synthase (EC 3.6.1.34) protein 8 - duckbill platypus mitochondrion
C:Species: mitochondrion Ornithorhynchus anatinus (duckbill platypus)
C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 20-Jun-2000
C:Accession: E58888
J:Janke, A.; Gemmell, N.J.; Feldmaier-Fuchs, G.; von Haeseler, A.; Paabo, S.
J. Mol. Evol. 42, 153-159, 1996
A:Title: The mitochondrial genome of a monotreme--the platypus (Ornithorhynchus anati
A:Reference number: A58888; MUID:97077300
A:Accession: E58888
A:Status: nucleic acid sequence not shown; translation not shown; not compared with C
A:Molecule type: DNA
A:Residues: 1-69 <JAN>
A:Cross-references: GB:X83427; NID:91469249; PIDN:CAA58459.1; PID:91469254
A:Note: Submitted to GenBank/EMBL/DBJ December, 1994
C:Genetics:
A:Map position: FOR7829-8038
A:Genome: mitochondrion
A:Genetic code: SCS1
C:Superfamily: H+-transporting ATP synthase protein 8
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 9.1%; Score 7; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 ARPSLLQ 75
|||||
DB 62 PPSLLIQ 68

RESULT 3

D72863
ACorf-107 protein - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, ACNPNV
A:Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C:Accession: D72863
R:Atres, M.D.; Howard, S.C.; Kuzlo, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A:Reference number: A72850; MUID:94303173
A:Accession: D72863
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <AYR>
A:Cross-references: GB:L22858; NID:9510708; PIDN:AAA66737.1; PID:9559176
C:Genetics:
A:Gene: ACorf-107

Query Match 9.1%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ARPSLL 73
|||||
DB 60 ARPSLL 66

RESULT 4

C95415
hypothetical protein SMA2279 [imported] - Sinorhizobium meliloti (strain 1021) magaplasma
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95415
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kaiman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9683-9688, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95462; MUID:21396509; PMID:11481432
A:Accession: C95415
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65885.1; PID:914524394; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chailu, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kloss, E.; Komp, C.; Lelaure,
Hubault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA2279
A:Genome: plasmid

Query Match 9.1%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCSTIAP 8
|||||
DB 28 TCSTIAP 34

RESULT 5

C86523
CT142 hypothetical protein_2 [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86523
R:Shitka, M.; Hiraoka, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: C86523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:BA000008; NID:98978632; PIDN:BAA98469.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPj0259

Query Match 9.1%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGLTSA 23
|||||
DB 74 ATGLTSA 80

RESULT 6

T41847
ACNPNV orf106 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BMSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T41847
R:Gomi, S.; Kajima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911
A:Accession: T41847
A:Status: preliminary; translated from GB/EMBL/DD8J
A:Molecule type: DNA
A:Residues: 1-249 <RAM>
A:Cross-references: EMBL:L33180; NID:93745835; PIDN:AMC63776.1; PID:93745929
A:Experimental source: isolate T3
C:Genetics:
A:Note: Orf_90

Query Match 9.1%; Score 7; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ARPSLL 73
|||||
DB 194 ARPSLL 200

RESULT 7

C89783
hypothetical protein SA0200 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89783
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: GB:BA000018; PID:g13700123; PIDN:BA841422.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0200

Query Match 9.1%; Score 7; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 LTSALNL 26
|||||||
DB 27 LTSALNL 33

RESULT 8
aICAR transformylase domain of purH-like protein [Imported] - Clostridium acetobutylicum
D97201
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97201
R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium CLO
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK80399.1; PID:g15025462; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2445

Query Match 9.1%; Score 7; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 17 ATGUTSA 23
|||||||
DB 58 ATGUTSA 64

RESULT 9
MFS permease [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AC2909
R:Wood, D.W.; Sebubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, M.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AC2909
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-425 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43689.1; PID:g17741216; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:

A:Gene: Atu2708
A:Map position: circular chromosome

Query Match 9.1%; Score 7; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TGSTIAP 8
|||||||
DB 390 TGSTIAP 396

RESULT 10
B97684
probable tartrate transporter AGR_C_4908 [Imported] - Agrobacterium tumefaciens (stra
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97684
R:Goodner, B.; Hinkie, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: B97684
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-487 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK8427.1; PID:g15157922; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_4908
A:Map position: circular chromosome

Query Match 9.1%; Score 7; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TGSTIAP 8
|||||||
DB 452 TGSTIAP 458

RESULT 11
T27668
hypothetical protein ZK1053.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T27668
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20402
A:Accession: T27668
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-536 <MIL>
A:Cross-references: EMBL:282084; PIDN:CAB04976.1; GSPDB:GN00019; CESP:ZK1053.2
A:Experimental source: clone ZK1053
C:Genetics:
A:Gene: CESP:ZK1053.2
A:Map position: 1;
A:Introns: 56/3; 88/3; 203/1; 228/2; 383/1; 467/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1053.2

Query Match 9.1%; Score 7; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 STIAPPT 10
|||||||
DB 295 STIAPPT 301

RESULT 12

probable DDAH ATP-dependent helicase - *Dichelobacter nodosus*
 C:Species: *Dichelobacter nodosus*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17395
 R:Billington, S.J.; Huggins, A.S.; Johannesen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, M.
 Infect. Immun. 67, 1277-1286, 1999
 A:Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) C
 A:Reference number: 218734; MUID:99150261
 A:Accession: T17395
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1965 <R1>
 A:Cross-references: EMBL:U20246; NID:g3493323; PID:g2317808; PIDN:MAC33384.1
 A:Experimental source: strain A198

Query Match

9.1%; Score 7; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ALNLPQV 29
 |||||
 Db 772 ALNLPQV 778

RESULT 13

HB3437
 hypothetical protein PA1669 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83437
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardly, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337
 A:Accession: H83437
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 11175 <STO>
 A:Cross-references: GB:AE004594; GB:AE004091; NID:g9947630; PIDN:AA05058.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1669

Query Match

9.1%; Score 7; DB 2; Length 1175;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 KRRRRAP 69
 |||||
 Db 213 KRRRRAP 219

RESULT 14

T17432
 Werner syndrome protein - mouse
 N:Alternate names: wrn protein
 C:Species: *Mus musculus* (house mouse)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17452
 R:Pepper, B.W.; Gayle, M.; Brady, M.; Swartz, A.; Gillett, L.A.; Allsich, R.S.; Mulligan,
 submitted to the EMBL data library, September 1998
 A:Description: Genomic structure of the human Werner's gene and cloning of its mouse hom
 A:Reference number: 218794
 A:Accession: T17452
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA

A:Residues: 11401 <PAE>
 A:Cross-references: EMBL:AF091215; NID:g3885837; PID:g3885838; PIDN:MAC78077.1
 C:Genetics:
 A:Gene: wrn

Query Match

9.1%; Score 7; DB 2; Length 1401;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 PPSLLQ 75
 |||||
 Db 1024 PPSLLQ 1030

RESULT 15

T30247
 Werner syndrome protein type1 - mouse
 N:Alternate names: wrn type1 protein
 C:Species: *Mus musculus* (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T30247
 R:Imamura, O.; Ichikawa, K.; Yamabe, Y.; Goto, M.; Sugawara, M.; Furuchi, Y.
 Genomics 41, 298-300, 1997
 A:Title: Cloning of a mouse homologue of the human Werner syndrome gene and assignmen
 A:Reference number: 220785; MUID:97288537
 A:Accession: T30247
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 111401 <IMA>
 A:Cross-references: EMBL:D86526; NID:g2130972; PIDN:BAA20269.1; PID:g2130973
 A:Experimental source: strain BALB/c; testis/spleen
 C:Genetics:
 A:Gene: WRN type1
 A:Map position: 8A4

Query Match

9.1%; Score 7; DB 2; Length 1401;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 PPSLLQ 75
 |||||
 Db 1024 PPSLLQ 1030

Search completed: June 21, 2002, 08:21:54
 Job time: 99 sec
